



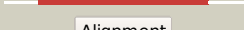

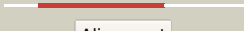




















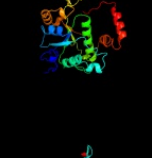

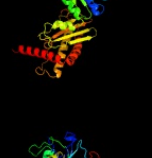
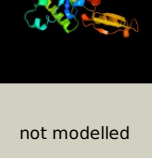


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0005_(gyrB)_5240_7267
Date	Tue Jul 23 14:50:03 BST 2019
Unique Job ID	8744ed81460bb9aa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6gauB_	 Alignment		100.0	99	PDB header: dna binding protein Chain: B: PDB Molecule: dna gyrase subunit b,dna gyrase subunit a; PDBTitle: extremely 'open' clamp structure of dna gyrase: role of the2 corynebacteriales gyrb specific insert
2	c4gfhA_	 Alignment		100.0	24	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2; PDBTitle: topoisomerase ii-dna-ampnp complex
3	c4i3hA_	 Alignment		100.0	51	PDB header: isomerase/dna Chain: A: PDB Molecule: topoisomerase iv subunit b, dna topoisomerase 4 subunit a PDBTitle: a three-gate structure of topoisomerase iv from streptococcus2 pneumoniae
4	c1zxnB_	 Alignment		100.0	21	PDB header: isomerase Chain: B: PDB Molecule: dna topoisomerase ii, alpha isozyyme; PDBTitle: human dna topoisomerase iia atpase/adp
5	c3lnuA_	 Alignment		100.0	35	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of pare subunit
6	c1qzrA_	 Alignment		100.0	22	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase ii; PDBTitle: crystal structure of the atpase region of saccharomyces cerevisiae2 topoisomerase ii bound to icrf-187 (dexrazoxane)
7	c5j5pB_	 Alignment		100.0	51	PDB header: isomerase/dna Chain: B: PDB Molecule: dna topoisomerase 4 subunit b; PDBTitle: amp-pnp-stabilized atpase domain of topoisomerase iv from2 streptococcus pneumoniae, complex type i
8	c1ei1B_	 Alignment		100.0	51	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase b; PDBTitle: dimerization of e. coli dna gyrase b provides a structural mechanism2 for activating the atpase catalytic center
9	c5btaD_	 Alignment		100.0	98	PDB header: isomerase/dna Chain: D: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of a topoisomerase ii complex
10	c1s16B_	 Alignment		100.0	39	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of e. coli topoisomerase iv pare 43kda subunit2 complexed with adpnp
11	c1kijB_	 Alignment		100.0	48	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of the 43k atpase domain of thermus thermophilus2 gyrase b in complex with novobiocin

12	c3cwwB_	Alignment		100.0	31	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase, b subunit, truncated; PDBTitle: crystal structure of b-subunit of the dna gyrase from myxococcus2 xanthus
13	c2xkjE_	Alignment		100.0	44	PDB header: isomerase Chain: E: PDB Molecule: topoisomerase iv; PDBTitle: crystal structure of catalytic core of a. baumannii topo iv (pare-2 parc fusion truncate)
14	c5eixB_	Alignment		100.0	43	PDB header: isomerase/dna Chain: B: PDB Molecule: dna topoisomerase 4 subunit b,dna topoisomerase 4 subunit PDBTitle: quinolone-stabilized cleavage complex of topoisomerase iv from2 klebsiella pneumoniae
15	c4hymA_	Alignment		100.0	39	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: topoisomerase iv, subunit b; PDBTitle: pyrrolopyrimidine inhibitors of dna gyrase b and topoisomerase iv,2 part i: structure guided discovery and optimization of dual targeting3 agents with potent, broad-spectrum enzymatic activity.
16	c4fm9A_	Alignment		100.0	30	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2-alpha; PDBTitle: human topoisomerase ii alpha bound to dna
17	c6ca8A_	Alignment		100.0	28	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 2; PDBTitle: crystal structure of plasmodium falciparum topoisomerase ii dna-2 binding, cleavage and re-ligation domain
18	c4tmaH_	Alignment		100.0	56	PDB header: isomerase/isomerase inhibitor Chain: H: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of gyrase bound to its inhibitor yacg
19	c3zm7E_	Alignment		100.0	99	PDB header: isomerase Chain: E: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of the atpase region of mycobacterium2 tuberculosis gyrb with amppcp
20	c2xcqA_	Alignment		100.0	63	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit b, dna gyrase subunit a; PDBTitle: the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
21	c5eixG_	Alignment	not modelled	100.0	47	PDB header: isomerase/dna Chain: G: PDB Molecule: dna topoisomerase 4 subunit b,dna topoisomerase 4 subunit PDBTitle: quinolone-stabilized cleavage complex of topoisomerase iv from2 klebsiella pneumoniae
22	c2xcsD_	Alignment	not modelled	100.0	66	PDB header: isomerase Chain: D: PDB Molecule: dna gyrase subunit b, dna gyrase subunit a; PDBTitle: the 2.1a crystal structure of s. aureus gyrase complex with gsk2994232 and dna
23	c4z2cD_	Alignment	not modelled	100.0	60	PDB header: isomerase Chain: D: PDB Molecule: dna gyrase subunit b; PDBTitle: quinolone(moxifloxacin)-dna cleavage complex of gyrase from s.2 pneumoniae
24	c3nuhB_	Alignment	not modelled	100.0	58	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
25	c3fofD_	Alignment	not modelled	100.0	53	PDB header: isomerase/dna Chain: D: PDB Molecule: dna topoisomerase 4 subunit b; PDBTitle: structural insight into the quinolone-dna cleavage complex2 of type iia topoisomerases
26	c2zjtB_	Alignment	not modelled	100.0	100	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of dna gyrase b' domain sheds lights on the2 mechanism for t-segment navigation
27	c1bjtA_	Alignment	not modelled	100.0	28	PDB header: topoisomerase Chain: A: PDB Molecule: topoisomerase ii; PDBTitle: topoisomerase ii residues 409-1201
28	d1bjta_	Alianment	not modelled	100.0	28	Fold: Type II DNA topoisomerase Superfamily: Type II DNA topoisomerase

						Family: Type II DNA topoisomerase
29	c3qx3B_	Alignment	not modelled	100.0	34	PDB header: isomerase/dna/isomerase inhibitor Chain: B: PDB Molecule: dna topoisomerase 2-beta; PDBTitle: human topoisomerase ii beta in complex with dna and etoposide
30	d1pvga2	Alignment	not modelled	100.0	24	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
31	d1ei1a2	Alignment	not modelled	100.0	52	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
32	d1kja2	Alignment	not modelled	100.0	50	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
33	d1s16a2	Alignment	not modelled	100.0	44	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
34	d1kja1	Alignment	not modelled	100.0	45	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
35	d1ei1a1	Alignment	not modelled	100.0	47	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
36	c4emvA_	Alignment	not modelled	100.0	54	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: dna topoisomerase iv, b subunit; PDBTitle: crystal structure of a topoisomerase atp inhibitor
37	c3g7bB_	Alignment	not modelled	100.0	56	PDB header: isomerase/isomerase inhibitor Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: staphylococcus aureus gyrase b co-complex with methyl ({5-[4-(4-2 hydroxypiperidin-1-yl)-2-phenyl-1,3-thiazol-5-yl]-1h-pyrazol-3-3 yl}methyl)carbamate inhibitor
38	c4geeA_	Alignment	not modelled	100.0	53	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: dna gyrase subunit b; PDBTitle: pyrrolopyrimidine inhibitors of dna gyrase b and topoisomerase iv,2 part i: structure guided discovery and optimization of dual targeting3 agents with potent, broad-spectrum enzymatic activity.
39	d1s16a1	Alignment	not modelled	100.0	30	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
40	d1s14a_	Alignment	not modelled	100.0	42	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
41	c4b6cB_	Alignment	not modelled	100.0	74	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b,dna gyrase subunit b,dna gyrase PDBTitle: structure of the m. smegmatis gyrb atpase domain in complex with an2 aminopyrazinamide
42	d1pvga1	Alignment	not modelled	100.0	20	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
43	c2q2eB_	Alignment	not modelled	99.9	18	PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b; PDBTitle: crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
44	c2zkbB_	Alignment	not modelled	99.9	13	PDB header: isomerase Chain: B: PDB Molecule: type 2 dna topoisomerase 6 subunit b; PDBTitle: crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
45	c1mx0D_	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit
46	c3h4IB_	Alignment	not modelled	99.9	18	PDB header: dna binding protein, protein binding Chain: B: PDB Molecule: dna mismatch repair protein pms1; PDBTitle: crystal structure of n terminal domain of a dna repair protein
47	d2hkja3	Alignment	not modelled	99.8	14	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
48	c3na3A_	Alignment	not modelled	99.8	15	PDB header: protein binding Chain: A: PDB Molecule: dna mismatch repair protein mlh1; PDBTitle: mutl protein homolog 1 isoform 1 from homo sapiens
49	d1b63a2	Alignment	not modelled	99.7	20	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
50	c1bkna_	Alignment	not modelled	99.6	17	PDB header: dna repair Chain: A: PDB Molecule: mutl; PDBTitle: crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
51	c1ea6A_	Alignment	not modelled	99.6	22	PDB header: dna repair Chain: A: PDB Molecule: pms1 protein homolog 2; PDBTitle: n-terminal 40kda fragment of nhpms2 complexed with adp PDB header: dna binding protein

52	c5x9yC_	Alignment	not modelled	99.5	19	Chain: C: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: crystal structure of the atpase domain from bacterial mismatch repair2 endonuclease aquifex aeolicus mutl.
53	d1h7sa2	Alignment	not modelled	99.5	19	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
54	d1bkna2	Alignment	not modelled	99.5	23	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
55	c3omuB_	Alignment	not modelled	99.2	15	PDB header: chaperone Chain: B: PDB Molecule: heat shock protein 83; PDBTitle: crystal structure of the n-terminal domain of an hsp90 from2 trypanosoma brucei, tb10.26.1080 in the presence of a3 thienopyrimidine derivative
56	c2akpA_	Alignment	not modelled	99.2	17	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: hsp90 delta24-n210 mutant
57	d2iwxa1	Alignment	not modelled	99.1	17	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
58	c2fwyA_	Alignment	not modelled	99.1	17	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp 90-alpha; PDBTitle: structure of human hsp90-alpha bound to the potent water2 soluble inhibitor pu-h64
59	c3iedA_	Alignment	not modelled	99.1	17	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein; PDBTitle: crystal structure of n-terminal domain of plasmodium falciparum hsp902 (pf14_0417) in complex with amppn
60	c1zwhA_	Alignment	not modelled	99.1	17	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: yeast hsp82 in complex with the novel hsp90 inhibitor radester amine
61	d1uyia_	Alignment	not modelled	99.1	16	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
62	d1uyma_	Alignment	not modelled	99.0	16	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
63	d1qy5a_	Alignment	not modelled	98.9	16	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
64	c2cg9A_	Alignment	not modelled	98.9	14	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
65	c2o1wB_	Alignment	not modelled	98.9	15	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic; PDBTitle: structure of n-terminal plus middle domains (n+m) of grp94
66	c3pehB_	Alignment	not modelled	98.9	16	PDB header: chaperone Chain: B: PDB Molecule: endoplasmic homolog; PDBTitle: crystal structure of the n-terminal domain of an hsp90 from plasmodium2 falciparum, pf11070c in the presence of a thienopyrimidine derivative
67	c4j0bB_	Alignment	not modelled	98.8	16	PDB header: chaperone Chain: B: PDB Molecule: tnf receptor-associated protein 1; PDBTitle: structure of mitochondrial hsp90 (trap1) with adp-bef3
68	c1y4sA_	Alignment	not modelled	98.8	15	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein htpg; PDBTitle: conformation rearrangement of heat shock protein 90 upon2 adp binding
69	c5fwkA_	Alignment	not modelled	98.8	15	PDB header: signaling protein Chain: A: PDB Molecule: heat shock protein hsp 90 beta; PDBTitle: atomic cryoem structure of hsp90-cdc37-cdk4 complex
70	c2iorA_	Alignment	not modelled	98.8	19	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of the n-terminal domain of htpg, the2 escherichia coli hsp90, bound to adp
71	c4ipeA_	Alignment	not modelled	98.7	16	PDB header: chaperone Chain: A: PDB Molecule: tnf receptor-associated protein 1; PDBTitle: crystal structure of mitochondrial hsp90 (trap1) with amppnp
72	c5tthA_	Alignment	not modelled	98.7	12	PDB header: chaperone Chain: A: PDB Molecule: c-terminal spycatcher fusion of wildtype zebrafish tnf PDBTitle: heterodimeric spycatcher/spytag-fused zebrafish trap1 in atp/adp-2 hybrid state
73	d2gqpa1	Alignment	not modelled	98.6	15	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Heat shock protein 90, HSP90, N-terminal domain
74	c5ulsA_	Alignment	not modelled	98.6	16	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of grp94 in the active conformation
						PDB header: chaperone

75	c2iopD_	Alignment	not modelled	98.6	16	Chain: D: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
76	c5ix1A_	Alignment	not modelled	98.5	17	PDB header: transcription Chain: A: PDB Molecule: morc family cw-type zinc finger protein 3; PDBTitle: crystal structure of mouse morc3 atpase-cw cassette in complex with2 amppnp and h3k4me3 peptide
77	c1y8oA_	Alignment	not modelled	98.4	17	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
78	c2q8fA_	Alignment	not modelled	98.3	20	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
79	c3tz5A_	Alignment	not modelled	98.3	25	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, PDBTitle: crystal structure of branched-chain alpha-ketoacid dehydrogenase2 kinase/phenylbutyrate complex with adp
80	c2bu8A_	Alignment	not modelled	98.3	13	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase kinase isoenzyme 2; PDBTitle: crystal structures of human pyruvate dehydrogenase kinase 2 containing2 physiological and synthetic ligands
81	c3crfB_	Alignment	not modelled	98.2	18	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase [lipoamide] kinase isozyme 2, PDBTitle: crystal structure of the pdhk2-l2 complex.
82	c3d2rB_	Alignment	not modelled	98.1	21	PDB header: transferase Chain: B: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; PDBTitle: crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
83	c1qjvA_	Alignment	not modelled	98.1	28	PDB header: transferase Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase; PDBTitle: branched-chain alpha-ketoacid dehydrogenase kinase (bck) complexed with2 atp-gamma-s
84	c4kp4B_	Alignment	not modelled	98.1	20	PDB header: transferase/signaling protein Chain: B: PDB Molecule: osmolarity sensor protein envz, histidine kinase; PDBTitle: deciphering cis-trans directionality and visualizing2 autophosphorylation in histidine kinases.
85	c5ofbB_	Alignment	not modelled	98.0	23	PDB header: nuclear protein Chain: B: PDB Molecule: morc family cw-type zinc finger protein 2; PDBTitle: crystal structure of human morc2 (residues 1-603) with spinal muscular2 atrophy mutation s871
86	d1jm6a2	Alignment	not modelled	98.0	16	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
87	c2o1uA_	Alignment	not modelled	98.0	16	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of full length grp94 with amp-pnp bound
88	c4ew8A_	Alignment	not modelled	97.8	22	PDB header: transferase Chain: A: PDB Molecule: sensor protein divl; PDBTitle: crystal structure of a c-terminal part of tyrosine kinase (divl) from2 caulobacter crescentus cb15 at 2.50 a resolution (psi community3 target, shapiro I.)
89	d1gkza2	Alignment	not modelled	97.8	22	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
90	c3d36B_	Alignment	not modelled	97.7	18	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: sporulation kinase b; PDBTitle: how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
91	c4u7nA_	Alignment	not modelled	97.7	16	PDB header: transferase Chain: A: PDB Molecule: histidine protein kinase sensor protein; PDBTitle: inactive structure of histidine kinase
92	c2c2aA_	Alignment	not modelled	97.6	26	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
93	c4i5sA_	Alignment	not modelled	97.6	18	PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase
94	c3sl2A_	Alignment	not modelled	97.4	21	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase yycg; PDBTitle: atp forms a stable complex with the essential histidine kinase walk2 (yycg) domain
95	d1th8a_	Alignment	not modelled	97.3	20	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
96	c4gczB_	Alignment	not modelled	97.3	18	PDB header: signaling protein, de novo protein Chain: B: PDB Molecule: blue-light photoreceptor, sensor protein fixl; PDBTitle: structure of a blue-light photoreceptor
97	c1b3qA_	Alignment	not modelled	97.3	20	PDB header: transferase Chain: A: PDB Molecule: protein (chemotaxis protein chea); PDBTitle: crystal structure of chea-289, a signal transducing histidine kinase
98	c5idjA_	Alignment	not modelled	97.2	26	PDB header: transferase Chain: A: PDB Molecule: cell cycle histidine kinase ccka; PDBTitle: bifunctional histidine kinase ccka (domains dhp-ca) in complex with2 adp/mg2+

99	c6blkB	Alignment	not modelled	97.2	21	PDB header: transferase Chain: B: PDB Molecule: signal transduction histidine-protein kinase/phosphatase PDBTitle: mycobacterial sensor histidine kinase mprb
100	c4r39A	Alignment	not modelled	97.1	28	PDB header: transferase Chain: A: PDB Molecule: blue-light-activated histidine kinase 2; PDBTitle: histidine kinase domain from erythrobacter litoralis el346 blue-light2 activated histidine kinase
101	c5idmA	Alignment	not modelled	97.0	26	PDB header: transferase Chain: A: PDB Molecule: cell cycle histidine kinase ccka; PDBTitle: bifunctional histidine kinase ccka (domain, ca) in complex with c-di-2 gmp and amppnp/mg2+
102	c2ch4A	Alignment	not modelled	97.0	22	PDB header: transferase/chemotaxis Chain: A: PDB Molecule: chemotaxis protein chea; PDBTitle: complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
103	c3a0tA	Alignment	not modelled	97.0	15	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: catalytic domain of histidine kinase thka (tm1359) in complex with adp2 and mg ion (trigonal)
104	d2c2aa2	Alignment	not modelled	96.9	28	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
105	c3a0rA	Alignment	not modelled	96.9	13	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
106	d1y8oa2	Alignment	not modelled	96.9	20	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
107	d1bxda	Alignment	not modelled	96.6	19	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
108	d1id0a	Alignment	not modelled	96.5	19	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
109	d1ysra1	Alignment	not modelled	96.5	20	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
110	c6dk8B	Alignment	not modelled	96.3	24	PDB header: signaling protein Chain: B: PDB Molecule: rets (regulator of exopolysaccharide and type iii PDBTitle: rets kinase region without cobalt
111	c3jz3B	Alignment	not modelled	96.1	34	PDB header: transferase Chain: B: PDB Molecule: sensor protein qsec; PDBTitle: structure of the cytoplasmic segment of histidine kinase qsec
112	d1i58a	Alignment	not modelled	96.1	25	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
113	c6e95A	Alignment	not modelled	96.0	22	PDB header: signaling protein Chain: A: PDB Molecule: staphylococcus aureus agrc histidine kinase module fused to PDBTitle: chimeric structure of saccharomyces cerevisiae gcn4 leucine zipper2 fused to staphylococcus aureus agrc cytoplasmic histidine kinase3 module (dataset isotropically truncated by hkl2000)
114	c4biuB	Alignment	not modelled	95.9	22	PDB header: transferase Chain: B: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (orthorhombic form 1)
115	c3ehgA	Alignment	not modelled	95.7	24	PDB header: transferase Chain: A: PDB Molecule: sensor kinase (yocf protein); PDBTitle: crystal structure of the atp-binding domain of desk in complex with2 atp
116	c4r3aA	Alignment	not modelled	95.6	28	PDB header: signaling protein Chain: A: PDB Molecule: blue-light-activated histidine kinase 2; PDBTitle: erythrobacter litoralis el346 blue-light activated histidine kinase
117	c4qpkA	Alignment	not modelled	95.4	17	PDB header: signaling protein Chain: A: PDB Molecule: phosphotransferase; PDBTitle: 1.7 angstrom structure of a bacterial phosphotransferase
118	c4biyD	Alignment	not modelled	95.3	31	PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2)
119	c4fmtB	Alignment	not modelled	95.2	19	PDB header: transferase Chain: B: PDB Molecule: chpt protein; PDBTitle: crystal structure of a chpt protein (cc_3470) from caulobacter2 crescentus cb15 at 2.30 a resolution
120	c4gt8A	Alignment	not modelled	95.1	24	PDB header: transferase Chain: A: PDB Molecule: sensor protein vras; PDBTitle: crystal structure of the catalytic and atp-binding domain from vras in2 complex with adp